



DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.  
 FT NON\_TER 1  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 150 210  
 FT DISULFID 256 314 O-LINKED (GALNAC).  
 FT CARBONYL 105 105 REMOVED POST-TRANSLATIONALLY (PROBABLE).  
 FT MOD\_RES 336 336 Q -> R (IN B ALLELE).  
 FT VARIANT 163 163 T -> A (IN B ALLELE).  
 FT VARIANT 194 194 N -> D (IN B ALLELE).  
 FT VARIANT 300 300 M -> I (IN B ALLELE).  
 FT VARIANT 301 301 L -> S (IN REF. 2 AND 3).  
 FT CONFLICT 25 25 S -> P (IN REF. 2 AND 3).  
 FT CONFLICT 36 36 I -> T (IN REF. 2 AND 3).  
 FT SEQUENCE 239 336 AA; 36658 MW; 7d879662607c356e CRC64;

SQ

Query Match 74.2%; Score 1802; DB 1; Length 336;  
 Best Local Similarity 100.0%; Pred. No. 1..3e-118;  
 Matches 336; Conservative 0; Mismatches 0; Indels 0; gaps 0;

QY 119 AKTTPPSVYPLAPGGDTGSVTGLKGYPFPSSVTWNSGSLSSHTFPAL0SG 178

Db 1 AKTTPPSVYPLAPGGDTGSVTGLKGYPFPSSVTWNSGSLSSHTFPAL0SG 60

QY 179 PNLEGGSVTFIPPKDVKMISLTPKVKTCVWVDYSEDDPDVQISWVNNVNEVHTAQ0T 238

Db 61 LYTMSSSVTVPPSSTPQSQTVCVHASSSTVDPKLEPSPGP1STINPCPCKBCHKCPA 120

QY 239 PNLEGGSVTFIPPKDVKMISLTPKVKTCVWVDYSEDDPDVQISWVNNVNEVHTAQ0T 298

Db 121 PNLEGGSVTFIPPKDVKMISLTPKVKTCVWVDYSEDDPDVQISWVNNVNEVHTAQ0T 180

QY 299 HREDYNSTRIVSPLIQHODWMSSKEFKCKVNNNDLPSPTERTISKIGLVRAPOVYL 358

Db 181 HREDYNSTRIVSPLIQHODWMSSKEFKCKVNNNDLPSPTERTISKIGLVRAPOVYL 240

QY 359 PPPAQLSRKDVSCLCLVWGFNPQDISVETWSNGHTEENYKTDAPVLDSDGSYFIYSKLN 418

Db 241 PPPAQLSRKDVSCLCLVWGFNPQDISVETWSNGHTEENYKTDAPVLDSDGSYFIYSKLN 300

QY 419 MKTSWEKTDPSFCNVRHEGLKNVYIKKTTSRSPK 454

Db 301 MKTSWEKTDPSFCNVRHEGLKNVYIKKTTSRSPK 336

RESULT 2

GCBM\_MOUSE STANDARD; PRT; 405 AA.

ID GCBM\_MOUSE 201867;

DT 21-JUL-1996 (Rel. 01, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG GAMMA-2B CHAIN C REGION, MEMBRANE-BOUND FORM.

OS MUS musculus (mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC [NCBI-TaxId=10090];

RN [1]

RP SEQUENCE OF 335-405 FROM N.A.

RX MEDLINE=82115295; PubMed=6799207;

RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.;

RT "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";

RL Cell 26:19-27(1981).

CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IgG CONTAIN TWO mRNA SPECIES FOR Ig GAMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS, A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.

CC -!- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER Ig GAMA CHAINS.

CC -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-335 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.

CC -!- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.

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CC DR EMBL; J00462; AAB59659.1; ALT-INIT.

CC DR PIR; C02154; G3NSBM.

CC DR MGD; MGI:96445; IgH-3.

CC DR InterPro; IPR000495; -.

CC DR InterPro; IPR003406; -.

CC DR Pfam; PF0007; 19; 3.

CC DR PROSITE; PS00200; IG\_MHC; 1.

CC KW Immunoglobulin domain; Immunoglobulin C region; Transmembrane; Alternative splicing.

FT NON\_TER 1

FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 210 210 POTENTIAL.

FT DISULFID 256 314 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 352 369 DOMAIN 370 405 AA; 44330 MW; 8B93CF0A9B6D49FA CRC64;

Query Match 74.0%; Score 1797; DB 1; Length 405;

Best Local Similarity 100.0%; Pred. No. 3..6e-118;

Matches 335; Conservative 0; Mismatches 0; Indels 0; gaps 0;

QY 119 AKTTPPSVYPLAPGGDTGSVTGLKGYPFPSSVTWNSGSLSSHTFPAL0SG 178

Db 1 AKTTPPSVYPLAPGGDTGSVTGLKGYPFPSSVTWNSGSLSSHTFPAL0SG 60

QY 179 PNLEGGSVTFIPPKDVKMISLTPKVKTCVWVDYSEDDPDVQISWVNNVNEVHTAQ0T 238

Db 61 LYTMSSSVTVPPSSTPQSQTVCVHASSSTVDPKLEPSPGP1STINPCPCKBCHKCPA 120

QY 239 PNLEGGSVTFIPPKDVKMISLTPKVKTCVWVDYSEDDPDVQISWVNNVNEVHTAQ0T 358

Db 181 HREDYNSTRIVSPLIQHODWMSSKEFKCKVNNNDLPSPTERTISKIGLVRAPOVYL 240

QY 359 PPPAQLSRKDVSCLCLVWGFNPQDISVETWSNGHTEENYKTDAPVLDSDGSYFIYSKLN 418

Db 241 PPPAQLSRKDVSCLCLVWGFNPQDISVETWSNGHTEENYKTDAPVLDSDGSYFIYSKLN 300

|            |   |                     |                                  |                                  |
|------------|---|---------------------|----------------------------------|----------------------------------|
| QY         | 419 MKTSKWEKTDSEFSCNVRHGLKNVYLKKTISRSPG   | 453                 | FT DISULFID 27 82                | INTERCHAIN (WITH A HEAVY CHAIN). |
| Db         | 301 MKTSKWEKTDSEFSCNVRHGLKNVYLKKTISRSPG   | 335                 | FT DISULFID 107 107              | INTERCHAIN (WITH A HEAVY CHAIN). |
| RESULT     | 3   | FT DISULFID 110 110 | INTERCHAIN (WITH A HEAVY CHAIN). |                                  |
| GCAM_MOUSE | STANDARD;   | PRT; 330 AA.        | FT DISULFID 112 112              | INTERCHAIN (WITH A HEAVY CHAIN). |
| ID         | GCAA_MOUSE  |                     | FT DISULFID 144 204              |                                  |
| AC         | P01863;   |                     | FT DISULFID 250 308              |                                  |
| DT         | 21-JUL-1986 (Rel. 01, Created)  |                     | FT DISULFID 330 330              | REMOVED POST-TRANSLATIONALLY.    |
| DT         | 21-JUL-1986 (Rel. 01, last sequence update)   |                     | FT DISULFID 330 330              |                                  |
| DT         | 30-MAY-2000 (Rel. 39, Last annotation update)   |                     | FT DISULFID 330 330              |                                  |
| DE         | IG GAMMA-2A CHAIN C REGION, A ALLELE.   |                     | FT DISULFID 330 330              |                                  |
| OS         | Mus musculus (Mouse)  |                     | FT DISULFID 330 330              |                                  |
| OC         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |                     | FT DISULFID 330 330              |                                  |
| OC         | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  |                     | FT DISULFID 330 330              |                                  |
| OX         | NCBI_TAXID=10090;   |                     | FT DISULFID 330 330              |                                  |
| RN         | [1]   |                     | FT DISULFID 330 330              |                                  |
| RP         | SEQUENCE FROM N.A.  |                     | FT DISULFID 330 330              |                                  |
| RX         | MEDLINE=81076554; PubMed=6777755;   |                     | FT DISULFID 330 330              |                                  |
| RA         | Sikorav J.-L.; Auffray C.; Rougeon F.;  |                     | FT DISULFID 330 330              |                                  |
| RT         | "Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA.";   |                     | FT DISULFID 330 330              |                                  |
| RL         | Nucleic Acids Res. 8:3143-3155(1980).   |                     | FT DISULFID 330 330              |                                  |
| RN         | [2]   |                     | FT DISULFID 330 330              |                                  |
| RP         | SEQUENCE FROM N.A.  |                     | FT DISULFID 330 330              |                                  |
| RX         | MEDLINE=81198976; PubMed=6262729;   |                     | FT DISULFID 330 330              |                                  |
| RA         | Yamawaki-Katada Y.; Miyata T.; Honjo T.;  |                     | FT DISULFID 330 330              |                                  |
| RT         | "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";   |                     | FT DISULFID 330 330              |                                  |
| RT         | Nucleic Acids Res. 9:1365-1381(1981).   |                     | FT DISULFID 330 330              |                                  |
| RN         | [3]   |                     | FT DISULFID 330 330              |                                  |
| RP         | SEQUENCE FROM N.A.  |                     | FT DISULFID 330 330              |                                  |
| RX         | MEDLINE=81228894; PubMed=6787604;   |                     | FT DISULFID 330 330              |                                  |
| RA         | Ollier R.; Auffray C.; Marchamps C.; Rougeon F.;  |                     | FT DISULFID 330 330              |                                  |
| RT         | "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic family.";  |                     | FT DISULFID 330 330              |                                  |
| RT         | Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).   |                     | FT DISULFID 330 330              |                                  |
| RN         | [4]   |                     | FT DISULFID 330 330              |                                  |
| RP         | MYELOMA PROTEIN MOPC 173.   |                     | FT DISULFID 330 330              |                                  |
| RX         | MEDLINE=7417517; PubMed=4831970;  |                     | FT DISULFID 330 330              |                                  |
| RA         | Bourgois A.; Fougerousse M.; Rocca-Serra J.;  |                     | FT DISULFID 330 330              |                                  |
| RT         | "Determination of the primary structure of a mouse IgG2a immunoglobulin: amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";   |                     | FT DISULFID 330 330              |                                  |
| RT         | Eur. J. Biochem. 43:423-435(1974).  |                     | FT DISULFID 330 330              |                                  |
| RN         | [5]   |                     | FT DISULFID 330 330              |                                  |
| RP         | DISULFIDE BONDS.  |                     | FT DISULFID 330 330              |                                  |
| RX         | MEDLINE=3056887; PubMed=4565406;  |                     | FT DISULFID 330 330              |                                  |
| RA         | de Preval C.; Fougerousse M.;   |                     | FT DISULFID 330 330              |                                  |
| RT         | "Determination of the primary structure of the disulfide bridges. I. Immunoglobulin. Identification of the mouse gamma G2a RT Eur. J. Biochem. 30:452-462(1972)."   |                     | FT DISULFID 330 330              |                                  |
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| CC         | -----   |                     | FT DISULFID 330 330              |                                  |
| CC         | EMBL; PIR: A02152; G2MSA; InterPro: IPR00495; Pfam: PF00047; PROSITE: PS00290; IG_MHC: 1; KW: Immunoglobulin domain; Immunoglobulin C region.   |                     | FT DISULFID 330 330              |                                  |
| CC         | NON_TER 1   |                     | FT DISULFID 330 330              |                                  |
| FT         | DISULFID 15 15  |                     | FT DISULFID 330 330              | INTERCHAIN (WITH A LIGHT CHAIN). |
| RESULT     | 4   |                     | FT DISULFID 330 330              |                                  |
| GCAM_MOUSE | STANDARD;   | PRT; 399 AA.        | FT DISULFID 330 330              |                                  |
| ID         | GCAM_MOUSE  |                     | FT DISULFID 330 330              |                                  |
| AC         | P01865;   |                     | FT DISULFID 330 330              |                                  |
| DT         | 21-JUL-1986 (Rel. 01, created)  |                     | FT DISULFID 330 330              |                                  |
| DT         | 01-AUG-1991 (Rel. 19, last sequence update)   |                     | FT DISULFID 330 330              |                                  |
| DT         | 15-JUL-1999 (Rel. 38, last annotation update)   |                     | FT DISULFID 330 330              |                                  |
| DE         | IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.  |                     | FT DISULFID 330 330              |                                  |
| OS         | Mus musculus (Mouse)  |                     | FT DISULFID 330 330              |                                  |
| OC         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  |                     | FT DISULFID 330 330              |                                  |
| OX         | NCBI_TAXID=10090;   |                     | FT DISULFID 330 330              |                                  |
| RN         | [1]   |                     | FT DISULFID 330 330              |                                  |
| RP         | SEQUENCE FROM N.A.  |                     | FT DISULFID 330 330              |                                  |
| RX         | MEDLINE=8222190; PubMed=6283537;  |                     | FT DISULFID 330 330              |                                  |
| RA         | Yamawaki-Katada Y.; Nakai S.; Miyata T.; Honjo T.;  |                     | FT DISULFID 330 330              |                                  |
| RT         | "Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";  |                     | FT DISULFID 330 330              |                                  |
| RT         | Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).   |                     | FT DISULFID 330 330              |                                  |
| RL         | - ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IgG CONTAIN TWO mRNA SPECIES FOR IgG CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END. ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.   |                     | FT DISULFID 330 330              |                                  |
| CC         | -----   |                     | FT DISULFID 330 330              |                                  |
| CC         | -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF THE A ALLELE.  |                     | FT DISULFID 330 330              |                                  |
| CC         | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial   |                     | FT DISULFID 330 330              |                                  |

|   |  |                                     |  |
|---|--|-------------------------------------|--|
| CC  | entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ). | RT                                  | IgG2aa and IgG2ab alleles of the mouse. ";   |
| CC  |  | RL                                  | Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499 (1981).   |
| CC  |  | RN                                  | [2]  |
| DR  |  | RP                                  | SEQUENCE.  |
| DR  | EMBL; J00471; AAB59661.1; ALT_INIT.  | RX                                  | MEDLINE=82037777; PUBMED=6794027;  |
| DR  | PIR; A02154; G2MSAM.   | RA                                  | Dognin M.J.; Lawwerens M.; Strosberg A.D.;   |
| DR  | InterPro; IPR00061; -.   | RT                                  | "Multiple amino acid substitutions between murine gamma 2a heavy chain Fc regions of Ig1a and Ig1b allotypic forms. ";   |
| DR  | InterPro; IPR03006; -.   | RL                                  | Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035 (1981).   |
| DR  | PROSITE; PS00290; IG_MHC_1.  | CC                                  | -1- MISCELLANEOUS: THE SEQUENCE DIFERS FROM THAT OF THE A ALLELE, FROM BALB/C MICE, AT 15% OF THE POSITIONS.   |
| KW  | Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.   | CC                                  |  |
| FT  | NON_TER 1 1  | CC                                  |  |
| FT  | DISULFD 15 15  | CC                                  | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.  |
| FT  | DISULFD 27 82  | CC                                  | CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ). |
| FT  | DISULFD 107 107  | CC                                  |  |
| FT  | DISULFD 110 110  | CC                                  |  |
| FT  | DISULFD 112 112  | CC                                  |  |
| FT  | DISULFD 144 204  | CC                                  |  |
| FT  | DISULFD 250 308  | CC                                  |  |
| FT  | TRANSMEM 346 363   | CC                                  |  |
| FT  | DOMAIN 364 399   | CC                                  |  |
| FT  | CARBOHYD 180 180   | CC                                  |  |
| SQ  | SEQUENCE 399 AA; 44020 MW; 4C38138PFAED3FF0 CRC64;   | CC                                  |  |
| Query Match 58.3%; Score 1414; DB 1; Length 399; Best Local Similarity 78.5%; Pred. No. 1.7e-91; Matches 263; Conservative 30; Mismatches 36; Indels 6; Gaps 2; Non_TER 1 1 | DR   | EMBL; J00479; -; NOT_ANNOTATED_CDS. |  |
| Db 1 AKTTAPSVPVPLAPGCCDTGSVTGLCKLVKGYPESVTWNSGSSSVTIPFALLSG 60  | DR   | PIR; A02153; G2MSAB.                |  |
| Oy 179 LYTMSSSVTVPSSTWSQTVCSVARPASSTVDKKLEPSGPPISTINPCPCKECHKCPA 238  | DR   | InterPro; IPR000495; -.             |  |
| Db 61 LYTLSSSVTWSNTPSOSTICCNVAHPASSTRVKDIEKPRGP -TIKPCPPC---KCPA 114  | DR   | DR                                  |  |
| Oy 239 PNLEGGPSVFLFPPNIKDVLMISLAPKVKTCWVNDSEDDPDVQISMFWNVNEVHTAQQT 298  | DR   | EMBL; J00479; -; NOT_ANNOTATED_CDS. |  |
| Db 115 PNLGPGSPVLFPPKIKDVLMISLSPVTCWVWDSEDDPDVQISMFWNVNEVHTAQQT 174   | DR   | PIR; A02153; G2MSAB.                |  |
| Oy 299 HREDDNSTIRVSTLPIQHODWMSKEFKCKVNNDLPSPIERTSKIGLVRAQVYL 358  | DR   | InterPro; IPR000506; -.             |  |
| Db 175 HREDDNSTLRVPSALPIQHODWMSKEFKCKVNNDLPSPIERTSKIGLVRAQVYL 234   | DR   | DR                                  |  |
| Oy 359 PPPAEGDLRKVSLTCLWVGNGPDISVEMNSNGHEENYKTATPVLDGSGSYIYSKLN 418   | DR   | EMBL; J00479; -; NOT_ANNOTATED_CDS. |  |
| Db 235 PPPEERETTKKVTLCTMVTDFMPEDIYVEMTNNGKTELNYKNTTEPVLDSDGSFYWSKL 294  | DR   | PIR; A02153; G2MSAB.                |  |
| Oy 419 MKTSKWEKTDTSFCNVRCNRHEGKKNYKVKTTSRSPG 453  | DR   | InterPro; IPR000506; -.             |  |
| Db 295 VEKKVNRVNSCVTVHGLHNHHTKSFRTPG 329  | DR   | DR                                  |  |
| RESULT 5  | Qy 419 MKTSKWEKTDTSFCNVRCNRHEGKKNYKVKTTSRSPG 454   | DR                                  | EMBL; J00479; -; NOT_ANNOTATED_CDS.  |
| GCAB_MOUSE  | ACID GCAB_MOUSE STANDARD; PRT; 335 AA.   | DR                                  | PIR; A02153; G2MSAB.   |
| ID  | P01864; 21 JUL 1986 (Rel. 01, Last sequence update)  | DR                                  | InterPro; IPR000506; -.  |
| DT  | 21-JUL-1986 (Rel. 01, Last sequence update)  | DR                                  | DR   |
| DT  | 15-JUL-1999 (Rel. 38, Last annotation update)  | DR                                  | DR   |
| DE  | IG_GAMMA_2A CHAIN C REGION, B ALLELE.  | DR                                  | DR   |
| OS  | Mus musculus (Mouse)   | DR                                  | DR   |
| OC  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxId=10090; [1]   | DR                                  | DR   |
| RN  | SEQUENCE FROM N. A.  | DR                                  | DR   |
| RP  |  | DR                                  | DR   |
| RC  | STRAIN=C57BL/6;  | DR                                  | DR   |
| RX  | MEDLINE=82037851; PubMed=6170065;  | DR                                  | DR   |
| RA  | Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;   | DR                                  | DR   |
| RN  | "Multiple differences between the nucleic acid sequences of the  | DR                                  | DR   |

|                       |   |   |  |                             |
|-----------------------|---|---|--|-----------------------------|
| RP                    | SEQUENCE FROM N.A.  | CC  | between the Swiss Institute of Bioinformatics and the EMBL outstation -  |                             |
| RX                    | MEDLINE=9923738; PubMed=3149946;  | CC  | the European Bioinformatics Institute. There are no restrictions on its  |                             |
| RA                    | Brueggemann M;  | CC  | use by non profit institutions as long as its content is in no way   |                             |
| RT                    | "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";   | CC  | modified and this statement is not removed. Usage by and for commercial  |                             |
| RL                    | Gene 74:473-482(1988).  | CC  | entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> ) |                             |
| PTR                   | PS0018; PS0018  | CC  | or send an email to license@isb-sib.ch).   |                             |
| DR                    | InterPro; IPR00495; -.  | CC  | -----  |                             |
| DR                    | InterPro; IPR003006; -.   | CC  | -----  |                             |
| DR                    | Pfam; PF0047; ig_3.   | CC  | -----  |                             |
| DR                    | PROSITE; PS00290; IG_MHC_1.   | CC  | -----  |                             |
| DR                    | PS0018; PS0018  | CC  | -----  |                             |
| KW                    | Immunoglobulin domain; Immunoglobulin C region.   | CC  | -----  |                             |
| FT                    | NON_TER 1   | CC  | -----  |                             |
| FT                    | DISULFID 15   | INTERCHAIN (WITH A LIGHT CHAIN).                        | DR   | Pfam; PF00047; ig_3.        |
| FT                    | DISULFID 27   | INTERCHAIN (WITH A HEAVY CHAIN).                        | DR   | EMBL; X07189; CAA30169_1.   |
| FT                    | DISULFID 106  | INTERCHAIN (WITH A HEAVY CHAIN).                        | DR   | PIR; S00847; S00847.        |
| FT                    | DISULFID 109  | INTERCHAIN (WITH A HEAVY CHAIN).                        | DR   | InterPro; IPR00495; -.      |
| FT                    | DISULFID 112  | INTERCHAIN (WITH A HEAVY CHAIN).                        | DR   | InterPro; IPR003006; -.     |
| FT                    | DISULFID 115  | INTERCHAIN (WITH A HEAVY CHAIN).                        | DR   | PROSITE; PS00290; IG_MHC_1. |
| FT                    | DISULFID 147  | INTERCHAIN (WITH A HEAVY CHAIN).                        | DR   | NON_TER 1                   |
| FT                    | DISULFID 207  | INTERCHAIN (WITH A HEAVY CHAIN).                        | FT   | NON_TER 1                   |
| SQ                    | SEQUENCE 253  | INTERCHAIN (WITH A HEAVY CHAIN).                        | FT   | DOMAIN 98                   |
| SQ                    | SEQUENCE 333 AA;  | INTERCHAIN (WITH A HEAVY CHAIN).                        | FT   | DOMAIN 114                  |
| Query Match           | 54.7%   | Score 1326.5; DB 1; Length 333;                         | FT   | DOMAIN 223                  |
| Best Local Similarity | 73.6%   | Pred. No. 1.6e-85; Pred. No. 1.6e-85; Indels 5; Gaps 3; | FT   | CH1.                        |
| Matches               | 248;  | Conservative 34; Mismatches 50; Indels 5; Gaps 3;       | FT   | CH2.                        |
| Db                    | 1 AKTPPPSVVPLAPCGDTGSSVYLGCLVKGYPPESVTWNSSLSSVHTPALLQSG 178   | FT  | CH3.   |                             |
| Qy                    | 179 LYTMSSSVVPPSSWPSQTWCYAHAPSSTTVDKLE-PSGPSTINCPCKECKCKCP 237  | FT  | INTERCHAIN (WITH A LIGHT CHAIN).   |                             |
| Db                    | 61 LYTTISSTV-SSWPSQTWCYAHAPSSTTVDKLVCKVERNGGIG--HKCPTCCHKCP 116   | FT  | INTERCHAIN (WITH A HEAVY CHAIN).   |                             |
| Qy                    | 238 APNIEEGPSVFLFPNPKIYVLMISLTPKVTCVVVDYSEDPPDQVLSWVNNEVHTAQOT 297  | FT  | INTERCHAIN (WITH A HEAVY CHAIN).   |                             |
| Db                    | 117 VPELIGGPSVFLFPKPKDILLISQNAKYTCVYDVSEEDPVQFSWVNNEVHTAQOT 176   | FT  | INTERCHAIN (WITH A HEAVY CHAIN).   |                             |
| Qy                    | 298 THRDYNSTIRVWSTLPIQODWMASGKERCKVKNKDLSPERIPTISKIGLVRAPOVYI 357   | FT  | INTERCHAIN (WITH A HEAVY CHAIN).   |                             |
| Db                    | 177 PREQYNSITFRVPSVLPALQHODWMASGKEKCKVKNKDLSPERIPTISKIGLVRAPOVYI 316  | FT  | INTERCHAIN (WITH A HEAVY CHAIN).   |                             |
| Qy                    | 358 LPPPAEQLSRKDSLTCLVVGFGNDISVETWSNIGHTEEENYKDTAPVLDSDGSFYIYKL 417   | FT  | INTERCHAIN (WITH A HEAVY CHAIN).   |                             |
| Db                    | 237 MGPPTEQLEQTQVSLICLTSGLFLNDIGVETWSNIGHTIEKNYKNTEPVMQDSGSRFMSKL 296   | FT  | INTERCHAIN (WITH A HEAVY CHAIN).   |                             |
| Qy                    | 418 NMKSKWETDSDSCNVREGLKLYKLTISSPGK 454   | FT  | INTERCHAIN (WITH A HEAVY CHAIN).   |                             |
| Db                    | 1 NVERSRWDSRAPFVCSVVHEGLAHNNHVEKSISRPGK 333   | FT  | INTERCHAIN (WITH A HEAVY CHAIN).   |                             |
| RESULT                | 7   | SEQUENCE 329 AA;  | FT   | DISULFID 113                |
| GCC_RAT               | STANDARD:   | PRT; 329 AA.  | FT   | DISULFID 143                |
| AC                    | P20762;   | FT  | DISULFID 203   |                             |
| DT                    | 01-FEB-1991 (Rel. 17, created)  | FT  | DISULFID 249   |                             |
| DT                    | 01-FEB-1991 (Rel. 17, last sequence update)   | FT  | DISULFID 307   |                             |
| DT                    | 15-JUL-1999 (Rel. 38, last annotation update)   | FT  | DISULFID 307   |                             |
| DE                    | IG GAMMA-2C CHAIN C REGION.   | FT  | DISULFID 307   |                             |
| OS                    | Rattus norvegicus (Rat).  | FT  | DISULFID 307   |                             |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;   | FT  | DISULFID 307   |                             |
| OC                    | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.   | FT  | DISULFID 307   |                             |
| OX                    | NCB_TAXID=10116;  | FT  | DISULFID 307   |                             |
| RN                    | [1]   | SEQUENCE FROM N.A.                                      | FT   | DISULFID 307                |
| RP                    | SEQUENCE FROM N.A.  | FT  | DISULFID 307   |                             |
| RX                    | Medline=88166903; PubMed=312722;  | FT  | DISULFID 307   |                             |
| RA                    | Brueggemann M., Dalmastro-Galfre P., Waldmann H., Calabi F.,  | FT  | DISULFID 307   |                             |
| RT                    | "Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3."; | FT  | DISULFID 307   |                             |
| RL                    | Eur. J. Immunol. 18:317-319(1988).  | FT  | DISULFID 307   |                             |
| CC                    | This SWISS-PROT entry is copyright. It is produced through a collaboration  | FT  | DISULFID 307   |                             |
| RESULT                | 8   | SEQUENCE 294 VDTDSMRGDDIVTCVHEALHNHTQKNLRSRGK 329       | FT   | DISULFID 307                |
| GCC_RAT               | STANDARD:   | PRT; 329 AA.  | FT   | DISULFID 307                |
| ID                    | GC3_MOUSE   | FT  | DISULFID 307   |                             |
| ID                    | GC3_MOUSE   | FT  | DISULFID 307   |                             |
| AC                    | P22436;   | FT  | DISULFID 307   |                             |
| DT                    | 01-AUG-1991 (Rel. 19, created)  | FT  | DISULFID 307   |                             |
| DT                    | 01-AUG-1991 (Rel. 19, last sequence update)   | FT  | DISULFID 307   |                             |
| DT                    | 15-JUL-1999 (Rel. 38, last annotation update)   | FT  | DISULFID 307   |                             |
| DE                    | IG GAMMA-3 CHAIN C REGION, SECRETED FORM.   | FT  | DISULFID 307   |                             |
| OS                    | MUS musculus (Mouse).   | FT  | DISULFID 307   |                             |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;   | FT  | DISULFID 307   |                             |
| OC                    | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  | FT  | DISULFID 307   |                             |
| OX                    | NCB_TAXID=10090;  | FT  | DISULFID 307   |                             |
| RN                    | [1]   | SEQUENCE FROM N.A.                                      | FT   | DISULFID 307                |
| RP                    | Medline=85021161; PubMed=6092035;   | FT  | DISULFID 307   |                             |
| RA                    | Wels J.A., Word C.J., Rumm D., Der-Balan G.P., Martinez H.M.,   | FT  | DISULFID 307   |                             |
| CC                    |   | FT  | DISULFID 307   |                             |

RA Tucker P.W., Blattner F.R.;  
 RT "Structural analysis of the murine IgG3 constant region gene.";  
 RL EMB0 J. 3:2041-2046(1984).

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CC EMBL: J00451; :- NOT\_ANNOTATED\_CDS.  
 PIR: B02156; G3MSC.  
 DR Interpro; IPR000495; :-.  
 DR Interpro; IPR000306; :-.  
 DR Pfam; PF00047; ig; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 CC KW Immunoglobulin C region; Glycoprotein; Transmembrane;  
 KW Alternative splicing;  
 FT NON\_TER 1 97 CH1.  
 FT DOMAIN 98 113 HINGE.  
 FT DOMAIN 114 223 CH2.  
 FT DOMAIN 224 327 CH3.  
 SQ SEQUENCE 329 AA; 36228 MW; F4582717182BAD6 CRC64;

Query Match 48.2%; Score 1170; DB 1; Length 329;  
 Best Local Similarity 66.2%; Pred. No. 1.3e-4; Matches 221; Conservative 33; Mismatches 74; Indels 6; Gaps 1; Non\_TER 1 97 CH1.  
 FT DOMAIN 98 113 HINGE.  
 FT DOMAIN 114 223 CH2.  
 FT DOMAIN 224 327 CH3.  
 FT DOMAIN 345 362 POTENTIAL.  
 FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).  
 FT CONFLICT 333 333 E -> G (IN REF. 2).  
 FT CONFLICT 342 342 E -> Q (IN REF. 2).  
 FT CONFLICT 388 388 P -> F (IN REF. 2).  
 SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 47.8%; Score 1159; DB 1; Length 398;  
 Best Local Similarity 66.0%; Pred. No. 9.5e-4; Matches 219; Conservative 33; Mismatches 74; Indels 6; Gaps 1; Non\_TER 1 97 CH1.  
 FT DOMAIN 98 113 HINGE.  
 FT DOMAIN 114 223 CH2.  
 FT DOMAIN 224 327 CH3.  
 FT DOMAIN 345 362 POTENTIAL.  
 FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 399 429 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 430 459 CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 421 AA; 46429 MW; CF7F264B50A41B95 CRC64;

RESULT 9  
 GC3M\_MOUSE ID GC3M\_MOUSE STANDARD; PRT; 399 AA.  
 AC P03987;  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85027161; PubMed=6092053;  
 RA Wels J.A., Word C.J., Rhim D., Der-Balan G.P., Martinez H.M.,

RA Tucker P.W., Blattner F.R.;  
 RT "Structural analysis of the murine IgG3 constant region gene.";  
 RL EMB0 J. 3:2041-2046(1984).  
 [2]  
 RP SEQUENCE OF 328-398 FROM N.A.  
 RX RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J., Wall R.;  
 CC "The structure of the mouse immunoglobulin in gamma 3 membrane gene segment.", Nucleic Acids Res. 11:6775-6785(1993).  
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 CC EMBL: J00451; AAB59655.1; :-.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Interpro; IPR000495; :-.  
 DR Pfam; PF00047; ig; 3.  
 DR EMBL: V01526; CAA24767.1; ALT\_SEQ.  
 DR PIR; A02155; G3MSM.  
 DR Interpro; IPR000306; :-.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Immunglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.  
 FT NON\_TER 1 97 CH1.  
 FT DOMAIN 98 113 HINGE.  
 FT DOMAIN 114 223 CH2.  
 FT DOMAIN 224 327 CH3.  
 FT DOMAIN 345 362 POTENTIAL.  
 FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 399 429 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 430 459 CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 421 AA; 46429 MW; CF7F264B50A41B95 CRC64;

RESULT 10  
 GC3L\_MOUSE ID GC3L\_MOUSE STANDARD; PRT; 399 AA.  
 AC P03987;  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85027161; PubMed=6092053;  
 RA Wels J.A., Word C.J., Rhim D., Der-Balan G.P., Martinez H.M.,



|  |     |  |
|--|-----|--|
| Q  | 299 | HREDYNSTIRWVSNLPIHQDAMSGKEKCKVNKLDPSEPIERTISKLGIVRAPVYIL   |
| Q  | 359 | MEDLINE-8211255; PubMed=6799207;   |
| Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.; "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains."; Cell 26:19-27(1981).     |     |  |
| Q  | 419 | SEQUENCE OF 1-44 FROM N.A. MEDLINE-82222190; PubMed=6683537;   |
| Yanawaki-Karata Y., Nakai S., Miyata T., Honjo T.; "Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains"; Proc. Natl. Acad. Sci. U.S.A. 79:2621-2627(1982). |     |  |
| Q  | 359 | -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO mRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.  |
| Q  | 419 | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and/or commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch). |
| Q  | 359 | DT 01-FEB-1991 (Rel. 17, Last sequence update)   |
| Q  | 359 | DT 15-JUL-1999 (Rel. 38, Last annotation update)   |
| Q  | 359 | DE IG GAMMA-1 CHAIN C REGION.  |
| Q  | 359 | OS Rattus norvegicus (Rat).  |
| Q  | 359 | OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; RN [1]  |
| Q  | 359 | DR NCBI_TaxID=10116;   |
| Q  | 359 | DR PIR; PS0017; PS0017.  |
| Q  | 359 | DR InterPro; IPR000495; -.   |
| Q  | 359 | DR InterPro; IPR003006; -.   |
| Q  | 359 | DR Pfam; PF00047; ig_3.  |
| Q  | 359 | DR PROSITE; PS00290; IG_MHC; 1.  |
| Q  | 359 | DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; RUE   |
| Q  | 359 | FT NON_TER 1   |
| Q  | 359 | FT DOMAIN 1 97   |
| Q  | 359 | FT DOMAIN 1 98   |
| Q  | 359 | FT DOMAIN 1 112  |
| Q  | 359 | FT DOMAIN 1 219  |
| Q  | 359 | FT DOMAIN 1 219  |
| Q  | 359 | FT DOMAIN 220 325  |
| Q  | 359 | FT DISULFID 27 82  |
| Q  | 359 | FT DISULFID 102 102  |
| Q  | 359 | FT DISULFID 106 105  |
| Q  | 359 | FT DISULFID 109 109  |
| Q  | 359 | FT DISULFID 111 111  |
| Q  | 359 | FT DISULFID 140 200  |
| Q  | 359 | FT DISULFID 246 304  |
| Q  | 359 | FT CARBOHYD 176 35946 MW; 013BAB45ER49B9DA CRC64;  |
| Q  | 359 | SEQUENCE 326 AA;   |
| Q  | 419 | Query Match 47.2%; Score 1145; DB 1; Length 393; Best local Similarity 64.5%; Pred. No. 8-8e-73; Matches 216; Conservative 45; Mismatches 62; Indels 12; Gaps 4;   |
| Q  | 419 | Matches 208; Conservation 50; Mismatches 68; Indels 10; Gaps 3;  |
| Q  | 419 | Query Match 45.8%; Score 1112; DB 1; Length 326; Best local Similarity 61.9%; Pred. No. 1.4e-70; Matches 208; Conservative 50; Mismatches 68; Indels 10; Gaps 3;   |
| Q  | 119 | Query Match 45.8%; Score 1112; DB 1; Length 326; Best local Similarity 61.9%; Pred. No. 1.4e-70; Matches 208; Conservative 50; Mismatches 68; Indels 10; Gaps 3;   |
| Q  | 119 | AKTPPPSVYPLAPGCGDTGTGSSVTLGCLVKGYFPESTVTVWNSGLSSVHFPALQSG 178  |
| Q  | 119 | 1 AKTPPPSVYPLAPGSAAQTSNTSHVTLGCLVKGYFPEPVTVTVWNSGLSSVHFPALQSD 60   |
| Q  | 119 | LYTMSSSVTVPSSTWPSSQTVTCSVAHASSITVVDKKLEPSPGISTINPCPPCKECHCPA 238   |
| Q  | 119 | 61 LYTLSSSVTVPSSTWPSSQTVTCSVAHASSITVVDKKLEPSPGISTINPCPPCKECHCPA 238  |
| Q  | 119 | AKTPPPSVYPLAPGCGDTGTGSSVTLGCLVKGYFPESTVTVWNSGLSSVHFPALQSG 178  |
| Q  | 119 | 1 AEITAPPSVYPLAPGTAALKNSAVTLGCLVKGYFPEPVTVTVWNSGLSSVHFPALQSG 60  |
| Q  | 119 | LYTMSSSVTVPSSTWPSSQTVTCSVAHASSITVVDKKLEPSPGISTINPCPPCKECHCPA 238   |
| Q  | 119 | 61 LYTLSSSVTVPSSTWPSSQTVTCSVAHASSITVVDKKLEPSPGISTINPCPPCKECHCPA 238  |
| Q  | 239 | Db 1 AEITAPPSVYPLAPGCGDTGTGSSVTLGCLVKGYFPESTVTVWNSGLSSVHFPALQSG 60   |
| Q  | 239 | 239 PNLEGGPSVFTPPNPNIKVDMISLTPTKTVVVWDVSDDPDQISWNVNNYEVHTAQQT 298  |
| Q  | 239 | 114 SEVS---SVEFFPPPKPKDVLTITLPTKTVVVWDVSDDPDQISWNVNNYEVHTAQQT 298  |
| Q  | 239 | 114 SEVS---SVEFFPPPKPKDVLTITLPTKTVVVWDVSDDPDQISWNVNNYEVHTAQQT 298  |
| Q  | 239 | 171 PERQFNSTFRSESLPHQDLNGRFRCKTSAAPPSEKTIKSPKGRTQVPTM 230  |

|                       |   |  |                                   |
|-----------------------|---|--|-----------------------------------|
| QY                    | 359   | PPPAEQLSRKVSLTCLLVGGFNGPDI SVWTSNQHTEENYKDTAVLDSLGSYIYSKLN | 418                               |
| Db                    | 231   | SPTKEEMTQNVEVSITCMVKGYFPDPDVWQMQPOENYKNTPPMDTDGSYFLYSKLN   | 290                               |
| QY                    | 419   | MKTSKEKTSFSNCNRHEGKKNYKRTSRSPGK                            | 454                               |
| Db                    | 291   | VKKERKQWQGKNTFCVSLHGLRNHHPEKSLSHSPGK                       | 326                               |
| Db                    | 291   | VKKERKQWQGKNTFCVSLHGLRNHHPEKSLSHSPGK                       | 326                               |
| RESULT                | 13  | GCA_RAT  |                                   |
| ID                    | GCA_RAT   | STANDARD;  | PRT;                              |
| ID                    | P20760;   |  | 322 AA.                           |
| DT                    | 01-FEB-1991 (Rel. 17, Created)  |  |                                   |
| DT                    | 01-FEB-1991 (Rel. 17, Last sequence update)   |  |                                   |
| DT                    | 15-JUL-1999 (Rel. 38, Last annotation update)   |  |                                   |
| DE                    | IG GAMMA-2A CHAIN C REGION.   |  |                                   |
| OS                    | Rattus norvegicus (Rat).  |  |                                   |
| OC                    | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;   |  |                                   |
| RN                    | [1]   |  |                                   |
| RP                    | SEQUENCE FROM N.A. MEDLINE=89232738; PubMed=3149946;  |  |                                   |
| RA                    | Brueremann M.:  |  |                                   |
| RT                    | "Evolution of the rat immunoglobulin gamma heavy-chain gene family." Gene 74:473-482(1988).   |  |                                   |
| RL                    |   |  |                                   |
| CC                    |   |  |                                   |
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| CC                    |   |  |                                   |
| CC                    |   |  |                                   |
| DR                    | EMBL: M13804; AAA41376.1; ALT_INIT.   |  |                                   |
| DR                    | PIR; PS0019; PS0019.  |  |                                   |
| DR                    | InterPro; IPR000495; -.   |  |                                   |
| DR                    | InterPro; IPR003006; -.   |  |                                   |
| DR                    | Pfam; PF00047; 19; 2.   |  |                                   |
| DR                    | PROSITE; PS00290; IG_MHC; 1.  |  |                                   |
| DR                    | IMMUNOGLOBULIN DOMAIN: Immunoglobulin C region.   |  |                                   |
| FT                    | KW  |  |                                   |
| FT                    | NON_TER   | 1  | 1                                 |
| FT                    | DISULFID  | 27   | 82                                |
| FT                    | DISULFID  | 102  | 102                               |
| FT                    | DISULFID  | 105  | 105                               |
| FT                    | DISULFID  | 107  | 107                               |
| FT                    | DISULFID  | 136  | 196                               |
| FT                    | DISULFID  | 242  | 300                               |
| FT                    | CARBONYD  | 172  | 172                               |
| SO                    | SEQUENCE  | 322 AA;  | 35186 MW; E8EA136A9DB01EDB CRC64; |
| Query                 | Match   |  |                                   |
| Best Local Similarity | 45.3%   | Score  | 1100;                             |
| Matches               | 203;  | Pred. No.  | 9.3e-70;                          |
| Conservative          | 53;   | Length   | 322;                              |
| Mismatches            | 66;   | Indels   | 14;                               |
|                       |   | Gaps   | 2;                                |
| Oy                    | 119   | AKTTPPSVVPLAPGCGDTGGSSVTLGLCKGYPPESTVTWNNSLSSVHFPALLQSG    | 178                               |
| Db                    | 1   | AETTAPSVPVLAQPTALKNSNSVMTGCKYFPEPYTVWNSGAASSQVHPEAVLQSG    | 60                                |
| QY                    | 179   | LYTMSSSVTVPSSTWQSQTWCVAHPASSTVVDKLEPGSGPISTINPCPPCKECKCPA  | 238                               |
| Db                    | 61  | LTYLTISSVTPSSTSWSQAVTCVNAVBPASTKVKDVKV-----RECNPCGC        | 107                               |
| QY                    | 239   | PNLEGPSVTFEPNPKDVMLSLTKVTCVWWDVSEDDPVQISMVNNEVHTAQQT       | 298                               |
| Db                    | 108   | TGSEVS-SVRFIFPKTKDVLITLTQKVTVVWDISONDPEVFWFIDDVWHTAQTHA    | 166                               |
| QY                    | 299   | HREDYNSTIRVSTLPIQHODMSGEFKCKVNKLPLSPIERTISKIKGLVRAQVYL     | 358                               |
| Db                    |   | :  | :                                 |
| RESULT                | 14  | GCA_HUMAN  |                                   |
| ID                    | GCA_HUMAN   | STANDARD;  | PRT;                              |
| ID                    | P01857;   |  | 330 AA.                           |
| AC                    | 21-JUL-1986 (Rel. 01, Created)  |  |                                   |
| DT                    | 21-JUL-1986 (Rel. 01, Last sequence update)   |  |                                   |
| DT                    | 15-JUL-1999 (Rel. 38, Last annotation update)   |  |                                   |
| DE                    | IG GAMMA-1 CHAIN C REGION.  |  |                                   |
| DN                    | IGHG1.  |  |                                   |
| OS                    | Homo sapiens (Human).   |  |                                   |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;   |  |                                   |
| RN                    | [1]   |  |                                   |
| RP                    | SEQUENCE FROM N.A. MEDLINE=82274238; PubMed=6287432;  |  |                                   |
| RA                    | Ellison J.W., Benson B.J., Hood L.E.;   |  |                                   |
| RT                    | "The nucleotide sequence of a human immunoglobulin C gamma1 gene." Nucleic Acids Res. 10:4071-4079(1982).   |  |                                   |
| RN                    | [2]   |  |                                   |
| RP                    | SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). MEDLINE=71064024; PubMed=548771;  |  |                                   |
| RA                    | Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  |  |                                   |
| RA                    | Waxdal M.J., Edelman G.M.;  |  |                                   |
| RT                    | "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4." Biochemistry 9:3161-3170(1970).   |  |                                   |
| RN                    | [3]   |  |                                   |
| RP                    | SEQUENCE OF 136-329 (EU). MEDLINE=71054025; PubMed=5530842;   |  |                                   |
| RA                    | Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,   |  |                                   |
| RA                    | Edelman G.M.;   |  |                                   |
| RT                    | "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy chain cyanogen bromide fragments H5-H7." Biochemistry 9:3171-3181(1970).   |  |                                   |
| RN                    | [4]   |  |                                   |
| RP                    | SEQUENCE (MYELOMA PROTEIN NIe). MEDLINE=77070569; PubMed=826475;  |  |                                   |
| RA                    | Poortinga H., Hilschmann N.;  |  |                                   |
| RT                    | "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NiE). III. The tryptic chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure." Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).   |  |                                   |
| RN                    | [5]   |  |                                   |
| RP                    | SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS. MEDLINE=B3289131; PubMed=6884994;  |  |                                   |
| RA                    | Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;   |  |                                   |
| RT                    | Three-dimensional structural determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.; structure of crystallized monoclonal immunoglobulin IgG1 KOL, II.; Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  |  |                                   |
| RL                    | [6]   |  |                                   |
| RP                    | DISULFIDE BONDS. MEDLINE=71064027; PubMed=4923144;  |  |                                   |
| RA                    | Gall W.E., Edelman G.M.;  |  |                                   |
| RT                    | "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds." Biochemistry 9:3188-3195(1970).  |  |                                   |
| RL                    | [7]   |  |                                   |
| RP                    | DISULFIDE BONDS. MEDLINE=77070567; PubMed=1002129;  |  |                                   |
| RA                    | Dreker L., Schwarz J., Reichel W., Hilschmann N.;   |  |                                   |

RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nle), I: Purification and  
 RT characterization of the L- and H-chains, the  
 RL cyanogen bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [8]

X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RP MEDLINE=11208100; PubMed=236608;

RX RA Deisenhofer J.;

RT RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 RT aureus at 2.9- and 2.8-A resolution";

RT RL BIOCHEMISTRY 20:2361-2370(1981).

CC -!- MISCELLANEOUS: NLE HAS THE GIM(17) ALLOSTATIC MARKER, 97 K, & THE  
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)  
 CC MARKER & THE GIM (NON-1) MARKERS.

CC -!- MISCELLANEOUS: NLE ALSO DIFFERS IN THE AMIDATION STATES OF  
 CC 35,116,198,269 & 272.

CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES  
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES  
 CC 268-272.

CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF  
 CC RESIDUES 198,267/272.

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CC EMBL; J00228; AAC82527.1; ALT-INIT.

DR PIR: A02146; GHRI.

DR PDB; 1FC1; 15-JUL-92.

DR PDB; 1FC2; 15-JUL-92.

MM: 147100; -.

DR Interpro; IPR000495; -.

DR Interpro; IPR00006; -.

Pfam; PF00047; 19; 3.

DR PROSITE; PS00290; IG\_MHC; 2.

DR KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW 3D-structure.

FT NON\_TER 1 1

FT DOMAIN 1 98 CH1.

FT DOMAIN 99 110 HINGE.

FT DOMAIN 111 223 CH2.

FT DOMAIN 224 330 CH3.

FT DISULFD 27 83 INTERCHAIN (WITH LIGHT CHAIN).

FT DISULFD 103 103 INTERCHAIN (WITH HEAVY CHAIN).

FT DISULFD 109 109 INTERCHAIN (WITH HEAVY CHAIN).

FT DISULFD 112 112 INTERCHAIN (WITH HEAVY CHAIN).

FT DISULFD 144 204

FT DISULFD 250 308 N-LINKED (GLCNAC).  
 FT CARBOND 180 330 REMOVED POST-TRANSLATIONALLY.  
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 FT VARIANT 97 97 /FTId=VAR\_003886.  
 FT VARIANT 239 239 D -> E (IN GIM(NON-1) MARKER).  
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 FT VARIANT 241 241 /FTId=VAR\_003888.

PT STRAND 158 162

PT STRAND 163 164

PT STRAND 165 166

PT HELIX 130 134

PT TURN 136 137

PT STRAND 141 148

PT STRAND 123 126

PT HELIX 175 178

PT STRAND 183 190

PT HELIX 193 197

PT TURN 198 199

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 or send an email to license@isb-sib.ch).

Query Match 44.8%; Score 1087; DB 1; Length 330;  
 Best Local Similarity 60.8%; Pred. No. 7.7e-69; Mismatches 75; Indels 8; Gaps 3;  
 Matches 205; Conservative 49; MisMatches 75; Index 8; Gaps 3;

Qy 178 GLYTMSSSVTPPSSTWPSQTVCSTAHAPASSTVVKLLEPSSGP1STINPOCPCKECHKP 237

Db 61 GLYSLSVSVVTPPSSTGQTYICVNHNKPSTNTVKVKEPKSCDT-HTCPP-----CP 113

Qy 238 APNLEGGSVTFPPNPKDVMISLTPKVQCVVWDVSEDDPDQ1SWFVNNEHTAQO 297

Db 114 APELLGGPSVTFPPNPKDVMISLTPKVQCVVWDVSEDDPDQ1SWFVNNEHTAQO 173

Qy 298 THREDYNSTTRWVSLPIQHQDWMSGKEFKKVNNDLSPPIERTISKIGLVRAPOVYI 357

Db 174 PREEQNSTVYRVSIVLQVHDLANGKEYKKVSKNLPAPEKITSKAKGQPBRQVWT 233

Qy 358 LPPIAAEQLRSRKDVSIETCLAVUGFNPQGDISVETNSGHTEEWYKDTAPVLDSDGSFYISKL 417

Db 234 LPPSRDELTKIQVSLSCLVKGFPSDIAVEWESQOPENYKTPPVLDSDGSFLYSKL 293

Qy 418 NMKTSKWEKTDTSFSNCNRHEGGLKNYLLKTTTSRSGK 454

Db 294 TVDKSKRWQGNVFSCSYVMHEALHNHYTQKSLSLSPGK 330

RESULT 15

GC\_RABIT ID GC\_RABIT STANDARD; PRT; 323 AA.

AC P01870; DT 21-JUL-1986 (Rel. 01, Created)

AC P01870; DT 21-JUL-1986 (Rel. 01, Last sequence update)

AC P01870; DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 1G GAMMA CHAIN C REGION.

OS Oryctolagus cuniculus (rabbit); Chordata; Craniata: Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=84030930; PubMed=6311520;

RP Bernstein K.E., Alexander C.B., Mage R.G.;  
 RP "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant  
 RP F-I haplotype.";  
 RP Immunogenetics 18:387-397(1983).

RP [2]

RP SEQUENCE OF 1-128.

RX MEDLINE=76135469; PubMed=1243651;  
 RA Pratt D.M., Mole L.E.;  
 RT "Sequence studies on the constant region of the Fd sections of rabbit  
 immunoglobulin G of different allotype.";  
 RL Biochem. J. 151:337-349(1975).  
 RN [3]  
 RP SEQUENCE OF 88-266 FROM N.A.  
 RX MEDLINE=83299917; PubMed=6193512;  
 RA Martens C.L., Moore K.W., Steinberg M., Hood L., Knight K.L.;  
 RT "Heavy chain genes of rabbit IgG: Isolation of a cDNA encoding gamma  
 heavy chain and identification of two genomic C gamma genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
 RN [4]  
 RP SEQUENCE OF 132-161.  
 RX MEDLINE=7011015; PubMed=5461106;  
 RA Fruchtter R.G., Jackson S.A., Mole L.E., Porter R.R.;  
 RT "Sequence studies of the Fd section of the heavy chain of rabbit  
 immunoglobulin G.";  
 RL Biochem. J. 116:249-259(1970).  
 RN [5]  
 RP SEQUENCE OF 129-131 AND 155-322.  
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;  
 RL (IN) Killander J. (eds.);  
 RL Gamma globulins, Nobel Symp. 3, pp.109-127, Almqvist and Wiksell,  
 Stockholm (1967).  
 -!- MISCELLANEOUS: REF. 1 SEQUENCE HAS THE D12 ALLOPTIC MARKER,  
 104-THR, AND THE E14 MARKER, 185-THR. REF. 3 HAS THE D11 AND E15  
 MARKERS AND REF. 5 THE E15 MARKER.  
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 enties requires a license agreement (See <http://www.isb-sib.ch/annouc>  
 or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL: M16426; AAA31289.1; -.  
 DR PIR: A02161; GIHR.  
 DR InterPro: IPR000495; -.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; 19; 3.  
 DR PROSITE: PS00240; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1 1  
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 FT 185 185 T -> A (IN E15 MARKER).  
 FT 48 48 N -> E (IN REF. 2).  
 FT 71 71 V -> VPV (IN REF. 2).  
 CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).  
 FT 173 173 N -> D (IN REF. 5).  
 FT 187 187 Q -> E (IN REF. 3 AND 5).  
 FT 201 201 N -> D (IN REF. 5).  
 FT 218 218 Q -> E (IN REF. 5).  
 FT 233 233 E -> Q (IN REF. 5).  
 CONFLICT 246 246 N -> D (IN REF. 5).  
 FT 256 256 E -> G (IN REF. 5).  
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 FT 266 266 N -> D (IN REF. 5).  
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 Best Local Similarity 61.4%; Pred. No. 2.1e-68;  
 Matches 205; Conservative 48; Mismatches 62; Indels 19; Gaps 0  
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 Db 6 PSVYPLAPCGCGDTGGSVTLVGLKQYFPESVTVWNGSLSSVHFPALLO-SGLYT 65  
 183 SSSVTVPSTWPSOTVTCVSAHPASSTVDKLEPSCPISTINCPCKECHK--CPAPN 240

Search completed: June 18, 2001, 15:34:34  
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Best Local Similarity 61.4%; Pred. No. 2.1e-68;
Matches 205; Conservative 48; Mismatches 62; Indels 19; Gaps 4;

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Tue Jun 19 08:18:09 2001

us-09-653-755a-4.rsp